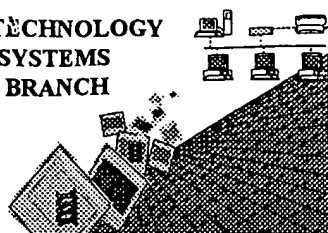


RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



RECEIVED
FEB 05 2002
TECH CENTER 1600/2800

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/724,254
Source: 1600
Date Processed by STIC: 1/26/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002



1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/724,254

DATE: 01/26/2002
TIME: 16:00:14

Input Set : A:\ES.txt
Output Set: N:\CRF3\01262002\I724254.raw

pr 1,5
**Does Not Comply
Corrected Diskette Needed**

5 <110> APPLICANT: RICCARDO DALLA-FAVERA
9 <120> TITLE OF INVENTION: ISOLATION OF FIVE NOVEL GENES CODING FOR NEW Fc RECEPTORS-

TYPE

10 MOLECULES INVOLVED IN THE PATHOGENESIS OF LYMPHOMA/MELANOMA
14 <130> FILE REFERENCE: 0575/58044-A/JPW/AJM
18 <140> CURRENT APPLICATION NUMBER: 09/724,254
20 <141> CURRENT FILING DATE: 2000-11-28
24 <160> NUMBER OF SEQ ID NOS: 55
28 <170> SOFTWARE: PatentIn version 3.0
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34 <211> LENGTH: 90
36 <212> TYPE: DNA
38 <213> ORGANISM: unknown *see item 11 on Error Summary Sheet*
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97 cctggagcag gcttccatgc tgccttgctg gcctttgctc cagtctgtgg 180

RAW SEQUENCE LISTING

DATE: 01/26/2002

PATENT APPLICATION: US/09/724,254

TIME: 16:00:14

Input Set : A:\ES.txt

Output Set: N:\CRF3\01262002\I724254.raw

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113 aaattgactg ctgtgaaaca atggcaatta tcatgcatg ggatatggag atgagaatga 660
115 tgtatttaga tcaaatttca aaataattaa aattcaagaa ctatttccac atccagagct 720
117 gaaagctaca gactctcagc ctacagaggg gaattctgta aacctgagct gtgaaacaca 780
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172 tcattagtga caaagatttg caacattaga gaaaagagac acaaatataa aattaaaaac 2400
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183 <212> TYPE: PRT

185 <213> ORGANISM: human

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191 <221> NAME/KEY: UNSURE

193 <222> LOCATION: (198)..(198)

195 <223> OTHER INFORMATION: x = any amino acid

201 <220> FEATURE:

203 <221> NAME/KEY: UNSURE

RAW SEQUENCE LISTING

DATE: 01/26/2002

PATENT APPLICATION: US/09/724,254

TIME: 16:00:14

Input Set : A:\ES.txt

Output Set: N:\CRF3\01262002\I724254.raw

205 <222> LOCATION: (513)..(513)

207 <223> OTHER INFORMATION: x= any amino acid

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221 Trp Thr Thr Phe Phe Lys Gly Glu Arg Val Thr Leu Thr Cys Asn Gly

222 35 40 45

224 Phe Gln Phe Tyr Ala Thr Glu Lys Thr Thr Trp Tyr His Arg His Tyr

225 50 55 60

227 Trp Gly Glu Lys Leu Thr Leu Thr Pro Gly Asn Thr Leu Glu Val Arg

228 65 70 75 80

230 Glu Ser Gly Leu Tyr Arg Cys Gln Ala Arg Gly Ser Pro Arg Ser Asn

231 85 90 95

236 Pro Val Arg Leu Leu Phe Ser Ser Asp Ser Leu Ile Leu Gln Ala Pro

237 100 105 110

239 Tyr Ser Val Phe Glu Gly Asp Thr Leu Val Leu Arg Cys His Arg Arg

240 115 120 125

242 Arg Lys Glu Lys Leu Thr Ala Val Lys Tyr Thr Trp Asn Gly Asn Ile

243 130 135 140

245 Leu Ser Ile Ser Asn Lys Ser Trp Asp Leu Leu Ile Pro Gln Ala Ser

246 145 150 155 160

248 Ser Asn Asn Asn Gly Asn Tyr Arg Cys Ile Gly Tyr Gly Asp Glu Asn

249 165 170 175

251 Asp Val Phe Arg Ser Asn Phe Lys Ile Ile Lys Ile Gln Glu Leu Phe

252 180 185 190

OK 254 Pro His Pro Glu Leu Xaa Ala Thr Asp Ser Gln Pro Thr Glu Gly Asn

255 195 200 205

257 Ser Val Asn Leu Ser Cys Glu Thr Gln Leu Pro Pro Glu Arg Ser Asp

258 210 215 220

260 Thr Pro Leu His Phe Asn Phe Phe Arg Asp Gly Glu Val Ile Leu Ser

261 225 230 235 240

263 Asp Trp Ser Thr Tyr Pro Glu Leu Gln Leu Pro Thr Val Trp Arg Glu

264 245 250 255

266 Asn Ser Gly Ser Tyr Trp Cys Gly Ala Glu Thr Val Arg Gly Asn Ile

267 260 265 270

269 His Lys His Ser Pro Ser Leu Gln Ile His Val Gln Arg Ile Pro Val

270 275 280 285

272 Ser Gly Val Leu Leu Glu Thr Gln Pro Ser Gly Gly Gln Ala Val Glu

273 290 295 300

275 Gly Glu Met Leu Val Leu Val Cys Ser Val Ala Glu Gly Thr Gly Asp

276 305 310 315 320

278 Thr Thr Phe Ser Trp His Arg Glu Asp Met Gln Glu Ser Leu Gly Arg

279 325 330 335

283 Lys Thr Gln Arg Ser Leu Arg Ala Glu Leu Glu Leu Pro Ala Ile Arg

284 340 345 350

286 Gln Ser His Ala Gly Gly Tyr Tyr Cys Thr Ala Asp Asn Ser Tyr Gly

287 355 360 365

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/724,254

DATE: 01/26/2002

TIME: 16:00:14

Input Set : A:\ES.txt

Output Set: N:\CRF3\01262002\I724254.raw

289 Pro Val Gln Ser Met Val Leu Asn Val Thr Val Arg Glu Thr Pro Gly
 290 370 375 380
 292 Asn Arg Asp Gly Leu Val Ala Ala Gly Ala Thr Gly Gly Leu Leu Ser
 293 385 390 395 400
 295 Ala Leu Ile Leu Ala Val Ala Leu Leu Phe His Cys Trp Arg Arg Arg
 296 405 410 415
 298 Lys Ser Gly Val Gly Phe Leu Gly Asp Glu Thr Arg Leu Pro Pro Ala
 299 420 425 430
 301 Pro Gly Pro Gly Glu Ser Ser His Ser Ile Cys Pro Ala Gln Val Glu
 302 435 440 445
 304 Leu Gln Ser Leu Tyr Val Asp Val His Pro Lys Lys Gly Asp Leu Val
 305 450 455 460
 307 Tyr Ser Glu Ile Gln Thr Thr Gln Leu Gly Glu Glu Glu Ala Asn
 308 465 470 475 480
 310 Thr Ser Arg Thr Leu Leu Glu Asp Lys Asp Val Ser Val Val Tyr Ser
 311 485 490 495
 313 Glu Val Lys Thr Gln His Pro Asp Asn Ser Ala Gly Lys Ile Ser Ser
 314 500 505 510

OK

316 Xaa Asp Glu Glu Ser

317 515

319 <210> SEQ ID NO: 6

321 <211> LENGTH: 2719

323 <212> TYPE: DNA

325 <213> ORGANISM: Human

330 <400> SEQUENCE: 6

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335	tcttggtctc	tgtcagtgga	cagtttgcaa	ggacacccag	gccattatt	ttcctccagc	180
337	ctccatggac	cacagtcttc	caaggagaga	gagtgacct	cacttgcaag	ggatttcgct	240
339	tctactcacc	acagaaaaca	aatggttacc	atcggtacct	tgggaaagaa	atactaagag	300
341	aaaccccgag	caatatacct	gaggttcagg	aatctggaga	gtacagatgc	caggcccagg	360
343	gtcctccctc	cagtagccct	gtgcaacttg	attttctctc	agcttcgctg	atcctgcaag	420
345	ctccactttc	tgtgtttgaa	ggagactctg	tggttctgag	gtgccgggca	aaggcggaag	480
347	taacactgaa	taatactatt	tacaagaatg	ataatgtcct	ggcattcctt	aataaaagaa	540
349	ctgacttcca	tattcctcat	gcatgtctca	aggacaatgg	tgcataatgc	tgtactggat	600
351	ataaggaaag	ttgttgccct	gtttcttcca	atacagtcaa	aatccaagtc	caagagccat	660
353	ttacacgtcc	agtgtgaga	gccagctcct	tccagcccat	cagcggggaa	ccagtgaacc	720
355	tgacctgtga	gacccagctc	tctctagaga	ggtcagatgt	cccgtccggg	ttccgtttct	780
357	tcagagatga	ccagaccctg	ggattaggct	ggagtctctc	cccgaatttc	cagattactg	840
359	ccatgtggag	taaagattca	gggttctact	gggtgaaggc	agcaacaatg	cctcacagcg	900
361	tcatactctg	cagcccgaga	tcctggatac	aggtgcagat	ccctgcatct	catcctgtcc	960
363	tcactctcag	ccctgaaaag	gctctgaatt	ttgaggggaa	caaggtgaca	cttcaactgtg	1020
365	aaaccccgag	agattctctg	cgcactttgt	acaggtttta	tcattgaggg	gtccccctga	1080
367	ggcacaagtc	agtcgcgtgt	gaaaggggag	catccatcag	cttctcactg	actacagaga	1140
369	attcagggaa	ctactactgc	acagctgaca	atggccttgg	cgccaagccc	agtaaggctg	1200
371	tgagcctctc	agtcactgtt	cccgtgtctc	atcctgtcct	caacctcagc	tctcctgagg	1260
373	acctgatttt	tgaggagacc	aaggtgacac	ttcactgtga	agcccagaga	ggttcaactcc	1320
375	ccatcctgta	ccagtttcat	catgaggatg	ctgccctgga	gcgtagggtc	gccaaactctg	1380
377	caggaggagt	ggccatcagc	ttctctctga	ctgcagagca	ttcaggggaa	tactactgca	1440

RAW SEQUENCE LISTING

DATE: 01/26/2002

PATENT APPLICATION: US/09/724,254

TIME: 16:00:14

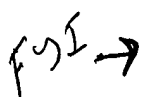
Input Set : A:\ES.txt

Output Set: N:\CRF3\01262002\I724254.raw

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391 cctcagggtt cccagggccc aggcctgtgg gggggacctg ctggagcttc actgtgaggc 1860
393 cccgagaggc tctcccccaa tctgtactg gttttatcat gaggatgtca ccctggggag 1920
395 cagctcagcc cctctggag gagaaagctt tttcaacctc tctctgactg cagaacattc 1980
397 tggaaactac tcatgtgagg ccaacaatgg cctagtggcc cagcacagtg acacaatatc 2040
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401 ggctgtggtg ggggacctgc tggagcttca ctgtgaggcc ctgagaggct cctccccaat 2160
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417 tttttagaac ataaactata ttctgaactg aaattattac atgaaaatga aaccaagaa 2640
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424 tctcattgac ttctaagaa 2719
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429 <211> LENGTH: 728
431 <212> TYPE: PRT
433 <213> ORGANISM: human
437 <400> SEQUENCE: 7
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440 1 5 10 15
442 Leu Thr Cys Lys Gly Phe Arg Phe Tyr Ser Pro Gln Lys Thr Lys Trp
443 20 25 30
445 Tyr His Arg Tyr Leu Gly Lys Glu Ile Leu Arg Glu Thr Pro Asp Asn
446 35 40 45
448 Ile Leu Glu Val Gln Glu Ser Gly Glu Tyr Arg Cys Gln Ala Gln Gly
449 50 55 60
451 Ser Pro Leu Ser Ser Pro Val His Leu Asp Phe Ser Ser Ala Ser Leu
452 65 70 75 80
454 Ile Leu Gln Ala Pro Leu Ser Val Phe Glu Gly Asp Ser Val Val Leu
455 85 90 95
457 Arg Cys Arg Ala Lys Ala Glu Val Thr Leu Asn Asn Thr Ile Tyr Lys
458 100 105 110
460 Asn Asp Asn Val Leu Ala Phe Leu Asn Lys Arg Thr Asp Phe His Ile
461 115 120 125
463 Pro His Ala Cys Leu Lys Asp Asn Gly Ala Tyr Arg Cys Thr Gly Tyr
464 130 135 140
466 Lys Glu Ser Cys Cys Pro Val Ser Ser Asn Thr Val Lys Ile Gln Val
467 145 150 155 160
471 Gln Glu Pro Phe Thr Arg Pro Val Leu Arg Ala Ser Ser Phe Gln Pro
472 165 170 175

```



Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

DATE: 01/26/2002

PATENT APPLICATION: US/09/724,254

TIME: 16:00:15

Input Set: A:\ES.txt

Output Set: N:\CRF3\01262002\I724254.raw

L:42 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:42 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:58 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:58 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:74 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:74 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:316 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:3032 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:3135 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
L:3432 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48
L:3548 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50
L:3551 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50
L:3630 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53
L:3765 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55
L:3768 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/724,254

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) 1-3 missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.